

SEQUENCE LISTING

<110> Egan, Sean E.
Wang, Wei
Sengar, Ameet

<120> ESE GENES AND PROTEINS

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<150> PCT/CA99/00375

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<150> US 60/118,739

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<170> PatentIn version 3.1

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cct Pro	tta Leu	tcc Ser	att Ile 180	cct Pro	tat Tyr	tct Ser	tct Ser	tca Ser 185	aca Thr	ttg Leu	cct Pro	cat His	gca Ala 190	tca Ser	tct Ser	576
tac Tyr	agc Ser	ctg Leu 195	atg Met	atg Met	gga Gly	gga Gly	ttt Phe 200	ggt Gly	ggt Gly	gct Ala	agt Ser	atc Ile 205	cag Gln	aag Lys	gcc Ala	624
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ctt Leu	cag Gln	tca Ser 275	aat Asn	ctc Leu	tct Ser	caa Gln	act Thr 280	cag Gln	cta Leu	gct Ala	act Thr	att Ile 285	tgg Trp	act Thr	ctg Leu	864
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625					630					635					640	
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cct Pro	aag Lys	aag Lys	gcc Ala	tta Leu	ctt Leu	cct Pro	cct Pro	aca Thr	gtg Val	tct Ser	ctc Leu	tct Ser	gct Ala	acc Thr	tca Ser	2400
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acc Thr	cgc Arg	act Thr	gtg Val	tcc Ser	cct Pro	gga Gly	tct Ser	gtg Val	tcc Ser	ccc Pro	att Ile	cac His	gga Gly	cag Gln	ggg Gly	2544
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865					870					875					880	
ctg Leu	gag Glu	cag Gln	cag Gln	gaa Glu	aac Asn	tgg Trp	tgg Trp	ttt Phe	ggg Gly	gag Glu	gtg Val	cac His	gga Gly	gga Gly	aga Arg	2688
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gac tac att gca ctt tat tca tac tca agt gta gag ccc ggg gat ttg Asp Tyr Ile Ala Leu Tyr Ser Tyr Ser Val Glu Pro Gly Asp Leu 945 950 955 960	2880
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acc aat ggt ctg act ggt ctc ttt cct tca aac tat gtt aag atg Thr Asn Gly Leu Thr Gly Leu Phe Pro Ser Asn Tyr Val Lys Met 1130 1135 1140	3429
aca aca gac tca gat cca agt caa cag tgg tgt gct gac ctc caa Thr Thr Asp Ser Asp Pro Ser Gln Gln Trp Cys Ala Asp Leu Gln 1145 1150 1155	3474
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 ile his glu leu ile gln thr glu glu arg tyr met asp asp leu
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<212> PRT

<213> Mus musculus

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Leu Gln Ser Gly Leu Pro Ala Pro Val Leu Ala Glu Ile Trp Ala Leu
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Ser Asp Leu Asn Lys Asp Gly Lys Met Asp Gln Gln Glu Phe Ser Ile
 65 70 75 80

Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Gln Gln Leu Pro Val
 85 90 95

Val Leu Pro Pro Ile Met Lys Gln Pro Pro Met Phe Ser Pro Leu Ile
 100 105 110

Ser Ala Arg Phe Gly Met Gly Ser Met Pro Asn Leu Ser Ile His Gln
 115 120 125

Pro Leu Pro Pro Val Ala Pro Ile Ala Thr Pro Leu Ser Ser Ala Thr
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Ser Gly Thr Ser Ile Pro Pro Leu Met Met Pro Ala Pro Leu Val Pro
 145 150 155 160

Ser Val Ser Thr Ser Ser Leu Pro Asn Gly Thr Ala Ser Leu Ile Gln
 165 170 175

Pro Leu Ser Ile Pro Tyr Ser Ser Ser Thr Leu Pro His Ala Ser Ser
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Tyr Ser Leu Met Met Gly Gly Phe Gly Gly Ala Ser Ile Gln Lys Ala
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Gln Ser Leu Ile Asp Leu Gly Ser Ser Ser Ser Thr Ser Ser Thr Ala
 210 215 220
 Ser Leu Ser Gly Asn Ser Pro Lys Thr Gly Thr Ser Glu Trp Ala Val
 225 230 235 240
 Pro Gln Pro Ser Arg Leu Lys Tyr Arg Gln Lys Phe Asn Ser Leu Asp
 245 250 255
 Lys Gly Met Ser Gly Tyr Leu Ser Gly Phe Gln Ala Arg Asn Ala Leu
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 Leu Gln Ser Asn Leu Ser Gln Thr Gln Leu Ala Thr Ile Trp Thr Leu
 275 280 285
 Ala Asp Ile Asp Gly Asp Gly Gln Leu Lys Ala Glu Glu Phe Ile Leu
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 Ala Met His Leu Thr Asp Met Ala Lys Ala Gly Gln Pro Leu Pro Leu
 305 310 315 320
 Thr Leu Pro Pro Glu Leu Val Pro Pro Ser Phe Arg Gly Gly Lys Gln
 325 330 335
 Val Asp Ser Val Asn Gly Thr Leu Pro Ser Tyr Gln Lys Thr Gln Glu
 340 345 350
 Glu Glu Pro Gln Lys Lys Leu Pro Val Thr Phe Glu Asp Lys Arg Lys
 355 360 365
 Ala Asn Tyr Glu Arg Gly Asn Met Glu Leu Glu Lys Arg Arg Gln Val
 370 375 380
 Leu Met Glu Gln Gln Gln Arg Glu Ala Glu Arg Lys Ala Gln Lys Glu
 385 390 395 400
 Lys Glu Glu Trp Glu Arg Lys Gln Arg Glu Leu Gln Glu Gln Glu Trp
 405 410 415
 Lys Lys Gln Leu Glu Leu Glu Lys Arg Leu Glu Lys Gln Arg Glu Leu
 420 425 430
 Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg Arg Glu
 435 440 445
 Ala Ala Lys Gln Glu Leu Glu Arg Gln Arg Arg Leu Glu Trp Glu Arg
 450 455 460
 Leu Arg Arg Gln Glu Leu Leu Ser Gln Lys Thr Arg Glu Gln Glu Asp
 465 470 475 480
 Ile Val Arg Leu Ser Ser Arg Lys Lys Ser Leu His Leu Glu Leu Glu
 485 490 495

Ala Val Asn Gly Lys His Gln Gln Ile Ser Gly Arg Leu Gln Asp Val
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 Gln Ile Arg Lys Gln Thr Gln Lys Thr Glu Leu Glu Val Leu Asp Lys
 515 520 525
 Gln Cys Asp Leu Glu Ile Met Glu Ile Lys Gln Leu Gln Gln Glu Leu
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 Lys Glu Tyr Gln Asn Lys Leu Ile Tyr Leu Val Pro Glu Lys Gln Leu
 545 550 555 560
 Leu Asn Glu Arg Ile Lys Asn Met Gln Leu Ser Asn Thr Pro Asp Ser
 565 570 575
 Gly Ile Ser Leu Leu His Lys Lys Ser Ser Glu Lys Glu Glu Leu Cys
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 Gln Arg Leu Lys Glu Gln Leu Asp Ala Leu Glu Lys Glu Thr Ala Ser
 595 600 605
 Lys Leu Ser Glu Met Asp Ser Phe Asn Asn Gln Leu Lys Glu Leu Arg
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 Glu Ser Tyr Asn Thr Gln Gln Leu Ala Leu Glu Gln Leu His Lys Ile
 625 630 635 640
 Lys Arg Asp Lys Leu Lys Glu Ile Glu Arg Lys Arg Leu Glu Gln Ile
 645 650 655
 Gln Lys Lys Lys Leu Glu Asp Glu Ala Ala Arg Lys Ala Lys Gln Gly
 660 665 670
 Lys Glu Asn Leu Trp Arg Glu Ser Ile Arg Lys Glu Glu Glu Lys
 675 680 685
 Gln Lys Arg Leu Gln Glu Glu Lys Ser Gln Asp Lys Thr Gln Glu Glu
 690 695 700
 Glu Arg Lys Ala Glu Ala Lys Gln Ser Glu Thr Ala Ser Ala Leu Val
 705 710 715 720
 Asn Tyr Arg Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met
 725 730 735
 Ser Phe Ser Ser Gly Asp Ile Ile Gln Val Asp Glu Lys Thr Val Gly
 740 745 750
 Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Lys Phe Gly Trp Phe
 755 760 765
 Pro Cys Asn Tyr Val Glu Lys Val Leu Ser Ser Glu Lys Ala Leu Ser
 770 775 780

Pro Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser
785 790 795 800

Thr Ser Ser Gln Pro Pro Ala Ser Val Thr Asp Tyr His Asn Val Ser
805 810 815

Phe Ser Asn Leu Thr Val Asn Thr Thr Trp Gln Gln Lys Ser Ala Phe
820 825 830

Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly
835 840 845

Gln Ala Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala
850 855 860

Lys Lys Glu Asn His Leu Asn Phe Ser Lys His Asp Val Ile Thr Val
865 870 875 880

Leu Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg
885 890 895

Gly Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Pro Gly Asn Glu Val
900 905 910

Gln Arg Gly Glu Pro Glu Ala Leu Tyr Ala Ala Val Thr Lys Lys Pro
915 920 925

Thr Ser Thr Ala Tyr Pro Val Thr Ser Thr Ala Tyr Pro Val Gly Glu
930 935 940

Asp Tyr Ile Ala Leu Tyr Ser Tyr Ser Ser Val Glu Pro Gly Asp Leu
945 950 955 960

Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys Asp Gly Glu
965 970 975

Trp Trp Thr Gly Ser Ile Gly Glu Arg Thr Gly Ile Phe Pro Ser Asn
980 985 990

Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser
995 1000 1005

Gly Ala Ser Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala
1010 1015 1020

Tyr Ala Ala Ser Gly Thr Glu Gln Leu Ser Leu Ala Pro Gly Gln
1025 1030 1035

Leu Ile Leu Ile Leu Lys Lys Asn Thr Ser Gly Trp Trp Gln Gly
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Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Lys Gly Trp Phe Pro
1055 1060 1065

Ala Ser His Val Lys Leu Leu Gly Pro Ser Ser Glu Arg Thr Met
1070 1075 1080

Pro Thr Phe His Ala Val Cys Gln Val Ile Ala Met Tyr Asp Tyr
1085 1090 1095

Met Ala Asn Asn Glu Asp Glu Leu Asn Phe Ser Lys Gly Gln Leu
1100 1105 1110

Ile Asn Val Met Asn Lys Asp Asp Pro Asp Trp Trp Gln Gly Glu
1115 1120 1125

Thr Asn Gly Leu Thr Gly Leu Phe Pro Ser Asn Tyr Val Lys Met
1130 1135 1140

Thr Thr Asp Ser Asp Pro Ser Gln Gln Trp Cys Ala Asp Leu Gln
1145 1150 1155

Ala Leu Asp Thr Met Gln Pro Thr Glu Arg Lys Arg Gln Gly Tyr
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<211> 738

<212> DNA

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35 40 45

Ala Arg Ser Gln Lys Thr Ser Gly Ile Gly Arg Leu Met Val His Val
50 55 60

Ile Glu Ala Thr Glu Leu Lys Ala Cys Lys Pro Asn Gly Lys Ser Asn
65 70 75 80

Pro Tyr Cys Glu Val Ser Met Gly Ser Gln Ser Tyr Thr Thr Arg Thr
85 90 95

Leu Gln Asp Thr Leu Asn Pro Lys Trp Asn Phe Asn Cys Gln Phe Phe
100 105 110

Ile Lys Asp Leu Tyr Gln Asp Val Leu Cys Leu Thr Met Phe Asp Arg
115 120 125

Asp Gln Phe Ser Pro Asp Asp Phe Leu Gly Arg Thr Glu Val Pro Val
130 135 140

Ala Lys Ile Arg Thr Glu Gln Glu Ser Lys Gly Pro Thr Thr Arg Arg
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Leu Gln Leu Phe Glu Gln Lys Thr Leu Leu
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<211> 309

<212> PRT

<213> Mus musculus

<400> 10

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35 40 45

Gln Arg Lys Gly Lys Gly Ala Val Gly Ala Tyr Gly Ser Glu Arg Thr
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Thr Gln Ser Leu Gln Asp Phe Pro Val Ala Asp Ser Glu Glu Glu Ala
65 70 75 80

Glu Glu Glu Phe Gln Lys Glu Leu Ser Gln Trp Arg Lys Asp Pro Ser
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 Gly Ser Lys Lys Lys Pro Lys Tyr Ser Tyr Lys Thr Val Glu Glu Leu
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 Lys Ala Lys Gly Arg Val Ser Lys Lys Leu Thr Ala Pro Gln Lys Glu
 115 120 125
 Leu Ser Gln Val Lys Val Ile Asp Met Thr Gly Arg Glu Gln Lys Val
 130 135 140
 Tyr Tyr Ser Tyr Ser Gln Ile Ser His Lys His Ser Val Pro Asp Glu
 145 150 155 160
 Gly Val Pro Leu Leu Ala Gln Leu Pro Pro Thr Ala Gly Lys Glu Ala
 165 170 175
 Arg Met Pro Gly Phe Ala Leu Pro Glu Leu Glu His Asn Leu Gln Leu
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 Gln Tyr Glu Arg Asp Met Val Val Ser Leu Ser His Glu Leu Glu Lys
 210 215 220
 Thr Ala Glu Val Leu Ala His Glu Glu Arg Val Ile Ser Asn Leu Ser
 225 230 235 240
 Lys Val Leu Ala Leu Val Glu Glu Cys Glu Arg Arg Met Gln Pro His
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 Gly Thr Asp Pro Leu Thr Leu Asp Glu Cys Ala Arg Ile Phe Glu Thr
 260 265 270
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<211> 97

<212> DNA

<213> Mus musculus

<400> 11

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<211> 123

<212> DNA

<213> Mus musculus

<400> 12

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<211> 140

<212> DNA

<213> Mus musculus

<400> 13

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gtctctctgc tggactatgg 140

<210> 14

<211> 2855

<212> DNA

<213> Mus musculus

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2855

<210> 15

<211> 1151

<212> DNA

<213> Mus musculus

<400> 15

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agccagagct gaatgctgcc atccccctctg ctaaccacagc aaagaccatg cagggcagcg	180
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<210> 16

<211> 382

<212> PRT

<213> Mus musculus

<400> 16

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 Ile Ala Leu Leu Cys Lys Pro Glu Pro Glu Leu Asn Ala Ala Ile Pro
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 50 55 60
 Leu Lys Ser Leu Leu Ser Asn Leu Asp Glu Ile Lys Lys Glu Arg Glu
 65 70 75 80
 Ser Leu Glu Asn Asp Leu Lys Ser Val Asn Phe Asp Met Thr Ser Lys
 85 90 95
 Phe Leu Thr Ala Leu Ala Gln Asp Gly Val Ile Asn Glu Glu Ala Leu
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 Ser Val Thr Glu Leu Asp Arg Ile Tyr Gly Gly Leu Thr Ser Lys Val
 115 120 125
 Gln Glu Ser Leu Lys Lys Gln Glu Gly Leu Leu Lys Asn Ile Gln Val
 130 135 140
 Ser His Gln Glu Phe Ser Lys Met Lys Gln Ser Asn Asn Glu Ala Asn
 145 150 155 160
 Leu Arg Glu Glu Val Leu Lys Asn Leu Ala Thr Ala Tyr Asp Asn Phe
 165 170 175
 Val Glu Leu Val Ala Asn Leu Lys Glu Gly Thr Lys Phe Tyr Asn Glu
 180 185 190
 Leu Thr Glu Ile Leu Val Arg Phe Gln Asn Lys Cys Ser Asp Ile Val
 195 200 205
 Phe Ala Arg Lys Thr Glu Arg Asp Glu Leu Leu Lys Asp Leu Gln Gln
 210 215 220
 Ser Ile Ala Arg Glu Pro Ser Ala Pro Ser Ile Pro Pro Pro Ala Tyr
 225 230 235 240
 Gln Ser Ser Pro Ala Ala Gly His Ala Ala Ala Pro Pro Thr Pro Ala
 245 250 255
 Pro Arg Thr Met Pro Pro Ala Lys Pro Gln Pro Pro Ala Arg Pro Pro
 260 265 270
 Pro Pro Val Leu Pro Ala Asn Arg Val Pro Pro Ala Ser Ala Ala Ala
 275 280 285
 Ala Pro Ala Gly Val Gly Thr Ala Ser Ala Ala Pro Pro Gln Thr Pro
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Gly Ser Ala Pro Pro Pro Gln Ala Gln Gly Pro Pro Tyr Pro Thr Tyr
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Pro Gly Tyr Pro Gly Tyr Cys Gln Met Pro Met Pro Met Gly Tyr Asn
325 330 335

Pro Tyr Ala Tyr Gly Gln Tyr Asn Met Pro Tyr Pro Pro Val Tyr His
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Gln Ser Pro Gly Gln Ala Pro Tyr Pro Gly Pro Gln Gln Pro Thr Tyr
355 360 365

Pro Phe Pro Gln Pro Pro Gln Gln Ser Tyr Tyr Pro Gln Gln
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<210> 17

<211> 1738

<212> DNA

<213> Mus musculus

<400> 17

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<210> 18

<211> 1521

<212> DNA

<213> Mus musculus

<220>

<221> misc_feature

<222> (102)..(103)

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<211> 720

<212> DNA

<213> Mus musculus

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<210> 20

<211> 801

<212> DNA

<213> Mus musculus

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<210> 21

<211> 119

<212> DNA

<213> Mus musculus

<400> 21

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<210> 22

<211> 5738

<212> DNA

<213> Mus musculus

<400> 22

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gtg Val	cat His 1535	gtc Val	att Ile	gaa Glu	gct Ala	aca Thr 1540	gaa Glu	tta Leu	aaa Lys	gcc Ala	tgc Cys 1545	aaa Lys	cca Pro	aac Asn	4644
ggg Gly	aaa Lys 1550	agt Ser	aat Asn	cca Pro	tac Tyr	tgt Cys 1555	gaa Glu	gtc Val	agc Ser	atg Met	ggc Gly 1560	tcc Ser	caa Gln	agc Ser	4689

tat acc acc agg acc ctg Tyr Thr 1565	cag gac aca cta aac ccc Gln Asp Thr Leu Asn Pro 1575	aag tgg aac Lys Trp Asn	4734
ttc aac tgc cag ttc ttc Phe Asn 1580	atc aag gat ctt tac cag Ile Lys Asp Leu Tyr Gln 1590	gac gtt ctg Asp Val Leu	4779
tgt ctc act atg ttt gac Cys Leu 1595	aga gac cag ttt tct cca Arg Asp Gln Phe Ser Pro 1605	gat gac ttc Asp Asp Phe	4824
ttg ggt cgt act gaa gtt Leu Gly 1610	cca gtg gca aaa atc cga Pro Val Ala Lys Ile Arg 1620	aca gaa cag Thr Glu Gln	4869
gaa agc aaa ggc ccc acc Glu Ser 1625	acc cgc cga cta cta ctg Thr Arg Arg Leu Leu Leu 1635	cac gaa gtc His Glu Val	4914
ccc act gga gaa gtc tgg Pro Thr 1640	gtc cgc ttt gac ctg Val Arg Phe Asp Leu 1650	caa ctt ttt gaa Gln Leu Phe Glu	4959
caa aaa act ctc ctt tga Gln Lys 1655			4977

<210> 27

<211> 1658

<212> PRT

<213> Mus musculus

<400> 27

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Ile Thr Ser Glu Glu Arg Thr Lys His Asp Lys Gln Phe Asp Asn Leu 20 25 30
Lys Pro Ser Gly Gly Tyr Ile Thr Gly Asp Gln Ala Arg Thr Phe Phe 35 40 45
Leu Gln Ser Gly Leu Pro Ala Pro Val Leu Ala Glu Ile Trp Ala Leu 50 55 60
Ser Asp Leu Asn Lys Asp Gly Lys Met Asp Gln Gln Glu Phe Ser Ile 65 70 75 80
Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Gln Gln Leu Pro Val 85 90 95
Val Leu Pro Pro Ile Met Lys Gln Pro Pro Met Phe Ser Pro Leu Ile 100 105 110
Ser Ala Arg Phe Gly Met Gly Ser Met Pro Asn Leu Ser Ile His Gln 115 120 125

Pro Leu Pro Pro Val Ala Pro Ile Ala Thr Pro Leu Ser Ser Ala Thr
 130 135 140
 Ser Gly Thr Ser Ile Pro Pro Leu Met Met Pro Ala Pro Leu Val Pro
 145 150 155 160
 Ser Val Ser Thr Ser Ser Leu Pro Asn Gly Thr Ala Ser Leu Ile Gln
 165 170 175
 Pro Leu Ser Ile Pro Tyr Ser Ser Ser Thr Leu Pro His Ala Ser Ser
 180 185 190
 Tyr Ser Leu Met Met Gly Gly Phe Gly Gly Ala Ser Ile Gln Lys Ala
 195 200 205
 Gln Ser Leu Ile Asp Leu Gly Ser Ser Ser Ser Thr Ser Ser Thr Ala
 210 215 220
 Ser Leu Ser Gly Asn Ser Pro Lys Thr Gly Thr Ser Glu Trp Ala Val
 225 230 235 240
 Pro Gln Pro Ser Arg Leu Lys Tyr Arg Gln Lys Phe Asn Ser Leu Asp
 245 250 255
 Lys Gly Met Ser Gly Tyr Leu Ser Gly Phe Gln Ala Arg Asn Ala Leu
 260 265 270
 Leu Gln Ser Asn Leu Ser Gln Thr Gln Leu Ala Thr Ile Trp Thr Leu
 275 280 285
 Ala Asp Ile Asp Gly Asp Gly Gln Leu Lys Ala Glu Glu Phe Ile Leu
 290 295 300
 Ala Met His Leu Thr Asp Met Ala Lys Ala Gly Gln Pro Leu Pro Leu
 305 310 315 320
 Thr Leu Pro Pro Glu Leu Val Pro Pro Ser Phe Arg Gly Gly Lys Gln
 325 330 335
 Val Asp Ser Val Asn Gly Thr Leu Pro Ser Tyr Gln Lys Thr Gln Glu
 340 345 350
 Glu Glu Pro Gln Lys Lys Leu Pro Val Thr Phe Glu Asp Lys Arg Lys
 355 360 365
 Ala Asn Tyr Glu Arg Gly Asn Met Glu Leu Glu Lys Arg Arg Gln Val
 370 375 380
 Leu Met Glu Gln Gln Gln Arg Glu Ala Glu Arg Lys Ala Gln Lys Glu
 385 390 395 400
 Lys Glu Glu Trp Glu Arg Lys Gln Arg Glu Leu Gln Glu Gln Glu Trp
 405 410 415

Lys Lys Gln Leu Glu Leu Glu Lys Arg Leu Glu Lys Gln Arg Glu Leu
 420 425 430
 Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg Arg Glu
 435 440 445
 Ala Ala Lys Gln Glu Leu Glu Arg Gln Arg Arg Leu Glu Trp Glu Arg
 450 455 460
 Leu Arg Arg Gln Glu Leu Leu Ser Gln Lys Thr Arg Glu Gln Glu Asp
 465 470 475 480
 Ile Val Arg Leu Ser Ser Arg Lys Lys Ser Leu His Leu Glu Leu Glu
 485 490 495
 Ala Val Asn Gly Lys His Gln Gln Ile Ser Gly Arg Leu Gln Asp Val
 500 505 510
 Gln Ile Arg Lys Gln Thr Gln Lys Thr Glu Leu Glu Val Leu Asp Lys
 515 520 525
 Gln Cys Asp Leu Glu Ile Met Glu Ile Lys Gln Leu Gln Gln Glu Leu
 530 535 540
 Lys Glu Tyr Gln Asn Lys Leu Ile Tyr Leu Val Pro Glu Lys Gln Leu
 545 550 555 560
 Leu Asn Glu Arg Ile Lys Asn Met Gln Leu Ser Asn Thr Pro Asp Ser
 565 570 575
 Gly Ile Ser Leu Leu His Lys Lys Ser Ser Glu Lys Glu Glu Leu Cys
 580 585 590
 Gln Arg Leu Lys Glu Gln Leu Asp Ala Leu Glu Lys Glu Thr Ala Ser
 595 600 605
 Lys Leu Ser Glu Met Asp Ser Phe Asn Asn Gln Leu Lys Glu Leu Arg
 610 615 620
 Glu Ser Tyr Asn Thr Gln Gln Leu Ala Leu Glu Gln Leu His Lys Ile
 625 630 635 640
 Lys Arg Asp Lys Leu Lys Glu Ile Glu Arg Lys Arg Leu Glu Gln Ile
 645 650 655
 Gln Lys Lys Lys Leu Glu Asp Glu Ala Ala Arg Lys Ala Lys Gln Gly
 660 665 670
 Lys Glu Asn Leu Trp Arg Glu Ser Ile Arg Lys Glu Glu Glu Lys
 675 680 685
 Gln Lys Arg Leu Gln Glu Glu Lys Ser Gln Asp Lys Thr Gln Glu Glu
 690 695 700

Glu Arg Lys Ala Glu Ala Lys Gln Ser Glu Thr Ala Ser Ala Leu Val
 705 710 715 720
 Asn Tyr Arg Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met
 725 730 735
 Ser Phe Ser Ser Gly Asp Ile Ile Gln Val Asp Glu Lys Thr Val Gly
 740 745 750
 Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Lys Phe Gly Trp Phe
 755 760 765
 Pro Cys Asn Tyr Val Glu Lys Val Leu Ser Ser Glu Lys Ala Leu Ser
 770 775 780
 Pro Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser
 785 790 795 800
 Thr Ser Ser Gln Pro Pro Ala Ser Val Thr Asp Tyr His Asn Val Ser
 805 810 815
 Phe Ser Asn Leu Thr Val Asn Thr Thr Trp Gln Gln Lys Ser Ala Phe
 820 825 830
 Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly
 835 840 845
 Gln Ala Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala
 850 855 860
 Lys Lys Glu Asn His Leu Asn Phe Ser Lys His Asp Val Ile Thr Val
 865 870 875 880
 Leu Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg
 885 890 895
 Gly Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Pro Gly Asn Glu Val
 900 905 910
 Gln Arg Gly Glu Pro Glu Ala Leu Tyr Ala Ala Val Thr Lys Lys Pro
 915 920 925
 Thr Ser Thr Ala Tyr Pro Val Thr Ser Thr Ala Tyr Pro Val Gly Glu
 930 935 940
 Asp Tyr Ile Ala Leu Tyr Ser Tyr Ser Ser Val Glu Pro Gly Asp Leu
 945 950 955 960
 Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys Asp Gly Glu
 965 970 975
 Trp Trp Thr Gly Ser Ile Gly Glu Arg Thr Gly Ile Phe Pro Ser Asn
 980 985 990

Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser
 995 1000 1005
 Gly Ala Ser Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala
 1010 1015 1020
 Tyr Ala Ala Ser Gly Thr Glu Gln Leu Ser Leu Ala Pro Gly Gln
 1025 1030 1035
 Leu Ile Leu Ile Leu Lys Lys Asn Thr Ser Gly Trp Trp Gln Gly
 1040 1045 1050
 Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Lys Gly Trp Phe Pro
 1055 1060 1065
 Ala Ser His Val Lys Leu Leu Gly Pro Ser Ser Glu Arg Thr Met
 1070 1075 1080
 Pro Thr Phe His Ala Val Cys Gln Val Ile Ala Met Tyr Asp Tyr
 1085 1090 1095
 Met Ala Asn Asn Glu Asp Glu Leu Asn Phe Ser Lys Gly Gln Leu
 1100 1105 1110
 Ile Asn Val Met Asn Lys Asp Asp Pro Asp Trp Trp Gln Gly Glu
 1115 1120 1125
 Thr Asn Gly Leu Thr Gly Leu Phe Pro Ser Asn Tyr Val Lys Met
 1130 1135 1140
 Thr Thr Asp Ser Asp Pro Ser Gln Gln Trp Cys Ala Asp Leu Gln
 1145 1150 1155
 Ala Leu Asp Thr Met Gln Pro Thr Glu Arg Lys Arg Gln Gly Tyr
 1160 1165 1170
 Ile His Glu Leu Ile Gln Thr Glu Glu Arg Tyr Met Asp Asp Asp
 1175 1180 1185
 Leu Gln Leu Val Ile Glu Val Phe Gln Lys Arg Met Ala Glu Glu
 1190 1195 1200
 Gly Phe Leu Thr Glu Ala Asp Met Ala Leu Ile Phe Val Asn Trp
 1205 1210 1215
 Lys Glu Leu Ile Met Ser Asn Thr Lys Leu Leu Arg Ala Leu Arg
 1220 1225 1230
 Val Arg Lys Lys Thr Gly Gly Glu Lys Met Pro Val Gln Met Ile
 1235 1240 1245
 Gly Asp Ile Leu Ala Ala Glu Leu Ser His Met Gln Ala Tyr Ile
 1250 1255 1260

Arg Phe Cys Ser Cys Gln Leu Asn Gly Ala Thr Leu Leu Gln Gln
 1265 1270 1275
 Lys Thr Asp Glu Asp Thr Asp Phe Lys Glu Phe Leu Lys Lys Leu
 1280 1285 1290
 Ala Ser Asp Pro Arg Cys Lys Gly Met Pro Leu Ser Ser Phe Leu
 1295 1300 1305
 Leu Lys Pro Met Gln Arg Ile Thr Arg Tyr Pro Leu Leu Ile Arg
 1310 1315 1320
 Ser Ile Leu Glu Asn Thr Pro Gln Ser His Val Asp His Ser Ser
 1325 1330 1335
 Leu Lys Leu Ala Leu Glu Arg Ala Glu Glu Leu Cys Ser Gln Val
 1340 1345 1350
 Asn Glu Gly Val Arg Glu Lys Glu Asn Ser Asp Arg Leu Glu Trp
 1355 1360 1365
 Ile Gln Ala His Val Gln Cys Glu Gly Leu Ala Glu Gln Leu Ile
 1370 1375 1380
 Phe Asn Ser Leu Thr Asn Cys Leu Gly Pro Arg Lys Leu Leu His
 1385 1390 1395
 Ser Gly Lys Leu Tyr Lys Thr Lys Ser Asn Lys Glu Leu His Ala
 1400 1405 1410
 Phe Leu Phe Asn Asp Phe Leu Leu Leu Thr Tyr Leu Val Arg Gln
 1415 1420 1425
 Phe Ala Ala Ala Ser Gly His Glu Lys Leu Phe Asn Ser Lys Ser
 1430 1435 1440
 Ser Ala Gln Phe Arg Met Tyr Lys Thr Pro Ile Phe Leu Asn Glu
 1445 1450 1455
 Val Leu Val Lys Leu Pro Thr Asp Pro Ser Gly Asp Glu Pro Val
 1460 1465 1470
 Phe His Ile Ser His Ile Asp Arg Val Tyr Thr Leu Arg Thr Asp
 1475 1480 1485
 Asn Ile Asn Glu Arg Thr Ala Trp Val Gln Lys Ile Lys Gly Ala
 1490 1495 1500
 Ser Glu Gln Tyr Ile Asp Thr Glu Lys Lys Lys Arg Glu Lys Ala
 1505 1510 1515
 Tyr Gln Ala Arg Ser Gln Lys Thr Ser Gly Ile Gly Arg Leu Met
 1520 1525 1530

Val His Val Ile Glu Ala Thr Glu Leu Lys Ala Cys Lys Pro Asn
1535 1540 1545

Gly Lys Ser Asn Pro Tyr Cys Glu Val Ser Met Gly Ser Gln Ser
1550 1555 1560

Tyr Thr Thr Arg Thr Leu Gln Asp Thr Leu Asn Pro Lys Trp Asn
1565 1570 1575

Phe Asn Cys Gln Phe Phe Ile Lys Asp Leu Tyr Gln Asp Val Leu
1580 1585 1590

Cys Leu Thr Met Phe Asp Arg Asp Gln Phe Ser Pro Asp Asp Phe
1595 1600 1605

Leu Gly Arg Thr Glu Val Pro Val Ala Lys Ile Arg Thr Glu Gln
1610 1615 1620

Glu Ser Lys Gly Pro Thr Thr Arg Arg Leu Leu Leu His Glu Val
1625 1630 1635

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1640 1645 1650

Gln Lys Thr Leu Leu
1655

<210> 28

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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<210> 29

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 29
gacagaggag cgtacatgg a

21

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 30
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<210> 31
<211> 51
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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<210> 32
<211> 37
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 32
cctggattac aaggatgatg atgacaaatg actcgag 37

<210> 33
<211> 21
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

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Ile Thr Val Glu Glu
20